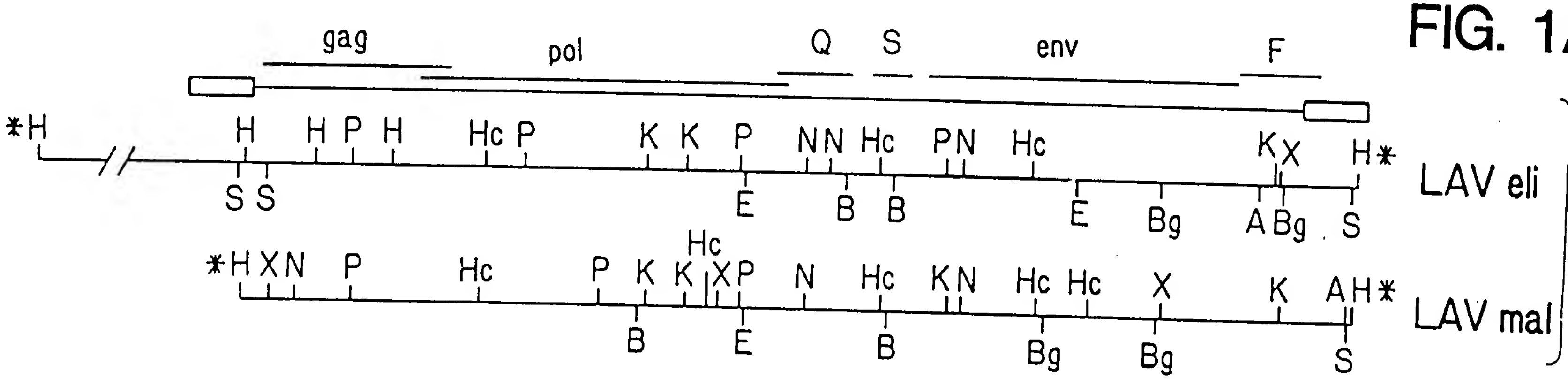
FIG. 1A



gag
pol
Q
S
env
F
*H
H
H
P
H
Hc
P
K
K
P
N
N
Hc
P
N
Hc
K
X
H*
S
S
E
B
B
E
Bg
A
Bg
S
LAV eli
*H
X
N
P
Hc
P
K
K
Hc
X
P
N
Hc
K
N
Hc
Hc
X
K
A
H*
B
E
B
Bg
Bg
S
LAV mal

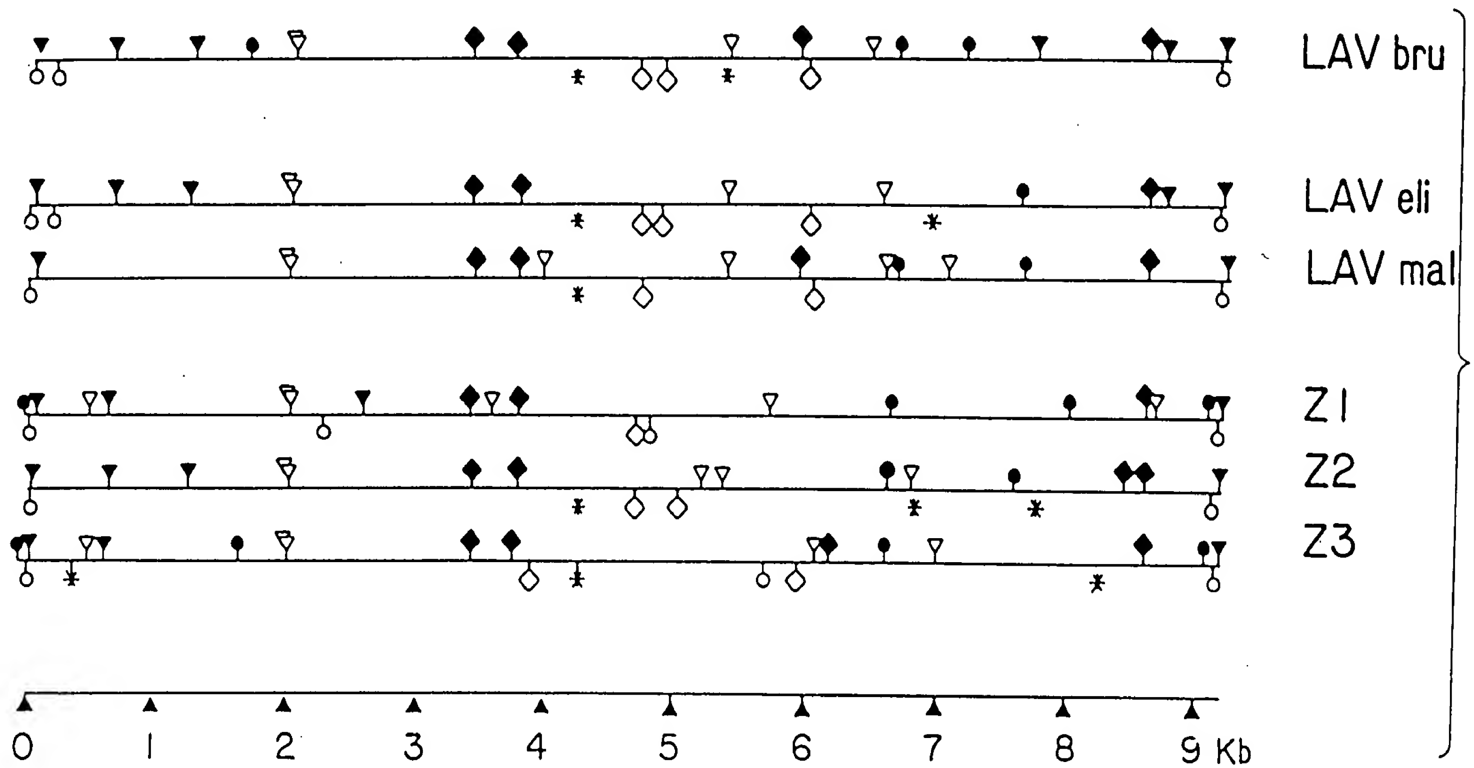
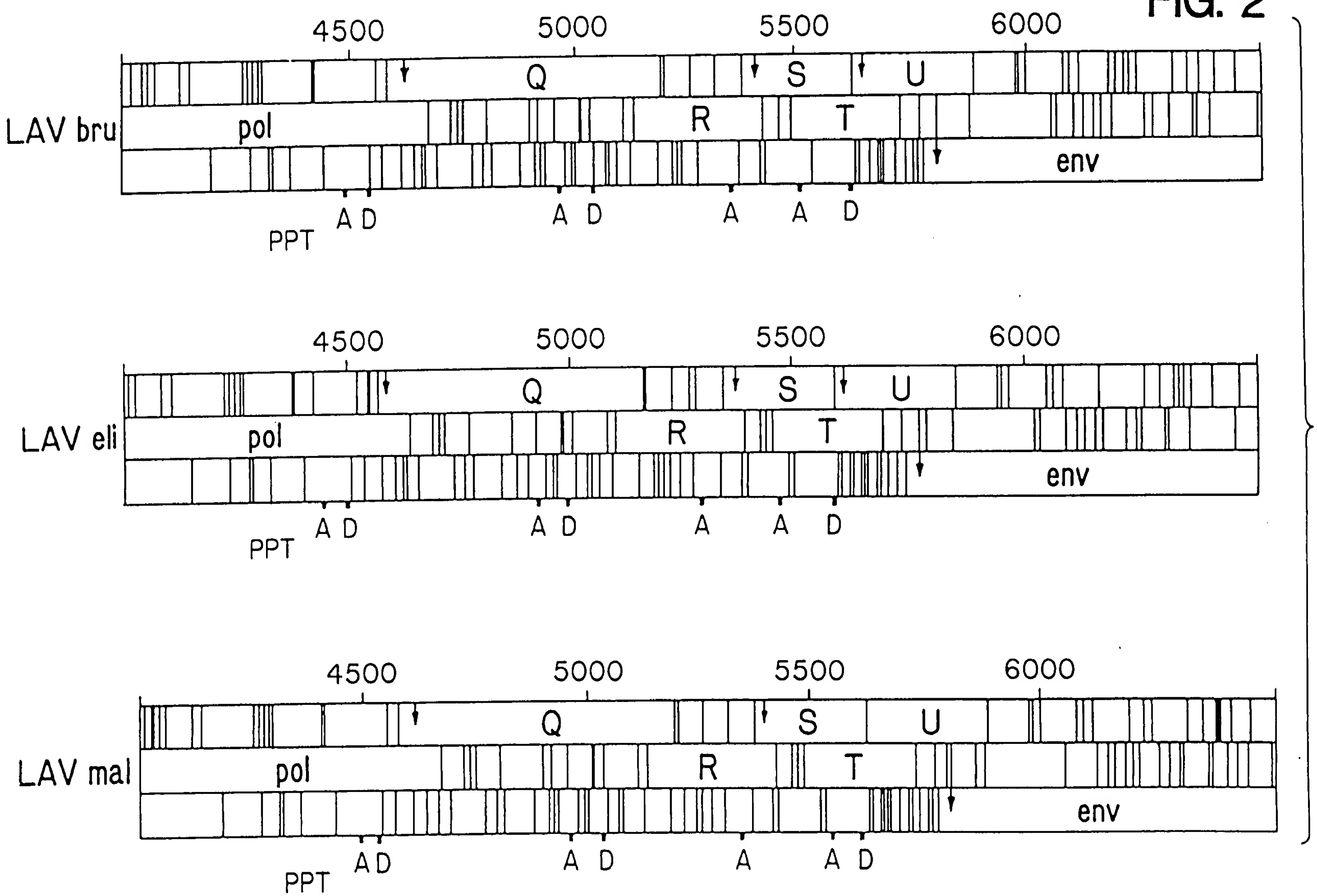


FIG. 1B

FIG. 2


LAV bru
LAV eli
LAV mal
4500
5000
5500
6000
Q
S
U
pol
R
T
env
A D
A D
A
A D
PPT

GAG

```
                  10         20         30         40         50         60         70         80
LAV BRU   MGARASVLSG GELDRWEKIR LRPGGKKKYK LKHIVWASRE LERFAVNPGL LETSEGCRQI LGQLQPSLQT GSEELRSLYN
ARV 2                    K               R    L            L        C   Q   ME   ST K      IK
LAV MAL               K  A               R               Y L            K   I     AI    T
LAV ELI               K  K               R

                                                                         p25
                                                                          ↓
                  90        100        110        120        130        140        150        160
LAV BRU   TVATLYCVHQ RIEIKDTKEA LDKIEEEQNK SKKKAQQAAA ------DTGH SSQVSQNYPI VQNIQGQMVH QAISPRTLNA
ARV 2                  DV        E                    ----AAG  N               L
LAV MAL                DV             I     RQ  T     AQQAAAA KN   S           A    I
LAV ELI            K G DV        E M                  ------   N N             L

                 170        180        190        200        210        220        230        240
LAV BRU   WVKVVEEKAF SPEVIPMFSA LSCGATPQDL NTMLNTVGGH QAAMQMLKET INEEAAEWDK VHPVHAGPIA PGQMREPRGS
ARV 2                                       M    I            D        D             P
LAV MAL       I                                                             L
LAV ELI       I

                 250        260        270        280        290        300        310        320
LAV BRU   DIAGTTSTLQ EQIGWMTNNP PIPVGEIYKR WIILGLNKIV RMYSPTSILD IRQGPKEPFR DYVDRFYKTL RAEQASQEVK
ARV 2                                                                                         D
LAV MAL                     S        D                     V                      F         T
LAV ELI                 A   S                 V            V                                  D
```

FIG. 3A-1

```
                                                                                    ↓p13
                 330        340        350        360        370        380        390        400

LAV BRU   NWMTETLLVQ NANPDCKTIL KALGPAATLE EMMTACQGVG GPGHKARVLA EAMSQVTNS- ATIMMQRGNF RNQRKIVKCF
ARV 2                                                                      P-   N              T
LAV MAL                                G                  S             A   T  A         KG - RI
LAV ELI                                Q                  S             A   V T A        KGP   I

                 410        420        430        440        450        460        470        480

LAV BRU   NCGKEGHIAR NCRAPRKKGC WKCGKEGHQM KDCTERQANF LGKIWPSYKG RPGNFLQSRP EPTAPPFLQS RPEPTAPPEE
ARV 2              K             R  R                                             ---- --------
LAV MAL          L                                           H                    ---- --------A
LAV ELI            K             R       L              R    H                    ---- --------A

                 490        500        510

LAV BRU   SFRSGVETTT PSQKQEPIDK ELYPLTSLRS LFGNDPSSQ
ARV 2      F   E K
LAV MAL     GF E IK-       QK        A  K       QL
LAV ELI     GF E I -       QK           K        L
```

FIG. 3A-2

Central Region: Q

```
                  10         20         30         40         50         60         70         80
LAV BRU   MENRWQVMIV WQVDRMRIRT WKSLVKHHMY VSGKARGWFY RHHYESPHPR ISSEVHIPLG DARLVITTYW GLHTGERDWH
ARV 2                                      I K  K           T    V            K               E
LAV MAL                          H           K  KN          R  K V               VR      Q   K
LAV ELI                      K               K  NR             K            E     K           E

                  90        100        110        120        130        140        150        160
LAV BRU   LGQGVSIEWR KKRYSTQVDP ELADQLIHLY YFDCFSDSAI RKALLGHIVS PRCEYQAGHN KVGSLQYLAL AALITPKKIK
ARV 2          A       K        G        H       E    KN I  YR                                 T
LAV MAL     H        Q      L   D                E     Q I          D                  T   A   TR
LAV ELI               R         G       M        E       I  D                          T   A  Q

                 170        180        190
LAV BRU   PPLPSVTKLT EDRWNKPQKT KGHRGSHTMN GH
ARV 2           K
LAV MAL         R            Q
LAV ELI         R            Q  R
```

FIG. 3B-1

```
               R

                      10         20         30         40         50         60         70         80

LAV BRU   MEQAPEDQGP QREPHNEWTL ELLEELKNEA VRHFPRIWLH GLGQHIYETY GDTWAGVEAI IRILQQLLFI HFRIGCRHSR
ARV 2                     Y               R          P     S   Y                                      Q
LAV MAL        A                          Q                S               E         S                Q
LAV ELI        A          Y   A           S                S               V                          Q

                      90

LAV BRU   IGVTQQRRAR -NGASRS
ARV 2       II        R
LAV MAL     I R       -  S
LAV ELI     IIR       -  S

               S (tat)
                      10         20         30         40         50         60         70

LAV BRU   MEPVDPRLEP WKHPGSQPKT ACTTCYCKKC CFHCQVCFTT KALGISYGRK KRRQRRRPPQ GSQTHQVSLS KQ
ARV 2           N             R     NN            YA    R  G                  A   D      A
LAV MAL    D    N      N      R   P NK         Y   M   I   G                       N A   DP P E
LAV ELI    D    N      N      R   P NK H       Y  P    LN  G                 G     G A    PIP
```

FIG. 3B-2

POL

```
                   10         20         30         40         50         60         70         80
LAV BRU   FFREDLAFLQ GKAREFSSEQ TRANSPTFSS EQTRANSPTR RELQVWGRDN NSLSEAGADR QGTVSFNFPQ ITLWQRPLVT
ARV 2                                  --- ---------         GE
LAV MAL       N   P        P           --- ---------S    R   G - KT   T  E   I    S           V
LAV ELI       N   P     G L PK         --- ---------S    R     -  P  KT  E                      A

                   90        100        110        120        130        140        150        160
LAV BRU   IKIGGQLKEA LLDTGADDTV LEEMSLPGRW KPKMIGGIGG FIKVRQYDQI LIEICGHKAI GTVLVGPTPV NIIGRNLLTQ
ARV 2      R                        N   K                       PV
LAV MAL   VRV                      IN   K                             K      I                M
LAV ELI                             N   K                       P     Q

                  170        180        190        200        210        220        230        240
LAV BRU   IGCTLNFPIS PIETVPVKLK PGMDGPKVKQ WPLTEEKIKA LVEICTEMEK EGKISKIGPE NPYNTPVFAI KKKDSTKWRK
ARV 2
LAV MAL                              R                T   KD        L
LAV ELI                                               T    D         R           I

                  250        260        270        280        290        300        310        320
LAV BRU   LVDFRELNKR TQDFWEVQLG IPHPAGLKKK KSVTVLDVGD AYFSVPLDED FRKYTAFTIP SINNETPGIR YQYNVLPQGW
ARV 2                                                         K
LAV MAL     N
LAV ELI                                                                 S
```

FIG. 3C-1

```
                 330        340        350        360        370        380        390        400
LAV BRU   KGSPAIFQSS MTKILEPFRK QNPDIVIYQY MDDLYVGSDL EIGQHRTKIE ELRQHLLRWG LTTPDKKHQK EPPFLWMGYE
ARV 2                                                                                   F
LAV MAL                       T K  E                                 E   K              F
LAV ELI                            EM                             K  E                  F R

                 410        420        430        440        450        460        470        480
LAV BRU   LHPDKWTVQP IVLPEKDSWT VNDIQKLVGK LNWASQIYPG IKVRQLCKLL RGTKALTEVI PLTEEAELEL AENREILKEP
ARV 2                 M                            A     K
LAV MAL               Q  D E                             K         A    DIV    A
LAV ELI            S  K    E         N  ER

                 490        500        510        520        530        540        550        560
LAV BRU   VHGVYYDPSK DLIAEIQKQG QGQWTYQIYQ EPFKNLKTGK YARTRGAHTN DVKQLTEAVQ KITTESIVIW GKTPKFKLPI
ARV 2       E          V                                  M                   VS          I
LAV MAL                                      QY           IKS                  AQ             R
LAV ELI                          H                        M            A     R S         R    R
```

FIG. 3C–2

```
                570        580        590        600        610        620        630        640
LAV BRU    QKETWETWWT EYWQATWIPE WEFVNTPPLV KLWYQLEKEP IVGAETFYVD GAASRETKLG KAGYVTNRGR QKVVTLTDTT
ARV 2            A  M                                                N            D      SIA
LAV MAL          A                                  T                N    K       D      S  E
LAV ELI             A                                  I             N            D      P

                650        660        670        680        690        700        710        720
LAV BRU    NQKTELQAIH LALQDSGLEV NIVTDSQYAL GIIQAQPDKS ESELVNQIIE QIIKKEKVYL AWVPAHKGIG GNEQVDKLVS
ARV 2                                                       S
LAV MAL                       S                          I          Q D     S
LAV ELI             N

                730        740        750        760        770        780        790        800
LAV BRU    AGIRKVLFLD GIDKAQDEHE KYHSNWRAMA SDFNLPPVVA KEIVASCDKC QLKGEAMHGQ VDCSPGIWQL DCTHLEGKVI
ARV 2               N       E                                                                I
LAV MAL    S                E                      I                                         I
LAV ELI    Q                E             N

                810        820        830        840        850        860        870        880
LAV BRU    LVAVHVASGY IEAEVIPAET GQETAYFLLK LAGRWPVKTI HTDNGSNFTS TTVKAACWWA GIKQEFGIPY NPQSQGVVES
ARV 2
LAV MAL    I                            I          VV            AA         N
LAV ELI                                            VV            AA
```

FIG. 3D–1

```
                      890        900        910        920        930        940        950        960
LAV BRU  MNKELKKIIG QVRDQAEHLK TAVQMAVFIH NFKRKGGIGG YSAGERIVDI IATDIQTKEL QKQITKIQNF RVYYRDSRDP
ARV 2      N                                          I M                              KK
LAV MAL       E                                                      I                 N
LAV ELI                                 RR            I

                      970        980        990       1000       1010
LAV BRU  LWKGPAKLLW KGEGAVVIQD NSDIKVVPRR KAKIIRDYGK QMAGDDCVAS RQDED
ARV 2                                                         G G
LAV MAL  I
LAV ELI  I                     K          V
```

FIG. 3D-2

```
ENV

                                 SP                                           OMP

                10        20        30          40        50        60        70        80
                                            ↓
LAV BRU   MRVK---EKY QHLWRWGWKW GTMLLGILMI CSATEKLWVT VYYGVPVWKE ATTTLFCASD AKAYDTEVHN VWATHACVPT
ARV 2      K  GTRRN             --- - L    M                                R
LAV MAL      REIQRN   NW        --- -M     M   T    IA D                      S E       I
LAV ELI     ARGIERNC  NW K      --- -I         T     ADN                      S E   A   I

                90       100       110       120       130       140       150       160

LAV BRU   DPNPQEVVLV NVTENFNMWK NDMVEQMHED IISLWDQSLK PCVKLTPLCV SLKCTDL-CN ATNTNSSNTN SSSGEMMME-
ARV 2              C             N      Q                         T N     - K         --- ----NWKE I
LAV MAL          IE E      G     N                                T N  NVN T  V GTNACS  RTNA LK  I
LAV ELI          IA E            N                                T N S E--L RN GTMG NV TTEEKG----

               170       180       190       200       210       220       230       240

LAV BRU   KGEIKNCSFN ISTSIRGKVQ KEYAFFYKLD IIPIDNDTTS -----YTLTS CNTSVITQAC PKVSFEPIPI HYCAPAGFAI
ARV 2                T    D I     N L RN   VV    AS T TNYTN R IN    R                        T
LAV MAL   -  V       TPVGSD R   -   T  N   LVQ  DSDN  ----S R IN                  T D
LAV ELI   ---M       VT VLKD K  QV  L  R    V      SST -NSTN R IN      A

               250       260       270       280       290       300       310       320

LAV BRU   LKCNKKTFNG TGPCTNVSTV QCTHGIRPVV STQLLLNGSL AEEEVVIRSA NFTDNAKTII VQLNQSVEIN CTRPNNNTRK
ARV 2                K                 I                         D   N          E A
LAV MAL       D K     EI K          K                      IM    E  L   T N        ET T       G    R
LAV ELI      RD K                                           I    E  L N   N   AH    E  K T   A  YQ   Q
```

FIG. 3E-1

```
                  330        340        350        360        370        380        390        400
                                          •                                                   •
BRU   SIRIQRGPGR AFVTIGK-IG NMRQAHCNIS RAKWNATLKQ IASKLREQFG NNKT-IIFKQ SSGGDPEIVT HSFNCGGEFF
2       Y --       W T RI   DI K         Q  N  E   VK             - V N          M      R
MAL   G HF--   Q LY T I-V   DI R Y T N ETE DK  Q   V V  GSLL- -   K   NS          T      R
ELI   RTP -- L Q SLY TKS-RS IIG          Q  SK  Q   V R  GTLL- -   I K  P          T

                  410        420        430        440        450        460        470        480
       •                                    •                                  •
BRU   YCNSTQLFNS TWFNSTWSTE CSNNTEGSDT ITLPCRIKQF INMWQEVGKA MYAPPISGQI RCSSNITGLL LTRDGGNN--
2        T     N  ------RLN RTEG K N     I       I                  C    S                T -V
MAL      TSK        Q NGARL- -  S  STGS          I      KT          A V  N L       I        NSSD
ELI      TSG        NI A NNI TES NSTNTN   Q      I   K VAGR-   I      ERN  L                I --

                                                                     TMP
                  490        500        510        520        530↓       540        550        560
BRU   NNGSEIFRPG GGDMRDNWRS ELYKYKVVKI EPLGVAPTKA KRRVVQREKR AVGI-GALFL GFLGAAGSTM GARSMTLTVQ
2     T DT V                       I       I                     V  M                  V L
MAL    SDN TL             I         R                    E     I L-  M                  A L
ELI    STN T                        Q          R         E     I L-  M                    V
```

FIG. 3E–2

```
                570        580        590        600        610        620        630        640
LAV BRU  ARQLLSGIVQ QQNNLLRAIE AQQHLLQLTV WGIKQLQARI LAVERYLKDQ QLLGIWGCSG KLICTTAVPW NASWSNKSLE
ARV 2                                              W        R
LAV MAL                                            W        Q   R   M       H    F     S    R  D
LAV ELI      M                                                                H    N     S    R  N

                650        660        670        680        690        700        710        720
LAV BRU  QIWNNMTWME WDREINNYTS LINSLIEESQ NQQEKNEQEL LELDKWASLW NWFNITNWLW YIKIFIMIVG GLVGLRIVFA
ARV 2    D  D     Q  E   D   N T YT L                              S
LAV MAL  D        Q  EK  S   G I YN       I      K                 S SK      R   IV     I    I
LAV ELI  E  Q        E   D   G   Y        T      K                 S  Q            I    I

                730        740        750        760        770        780        790        800
LAV BRU  VLSIVNRVRQ GYSPLSFQTH LPTPRGP-DR PEGIEEEGGE RDRDRSIRLV NGSLALIWDD LRSLCLFSYH RLRDLLLIVT
ARV 2                        R   V    -    D               V    D F     E           R         AA
LAV MAL     L             L  L        P              QG G         FS         N                A
LAV ELI     L                L   A    -      T        G    V  L   FS                       I  AV

                810        820        830        840        850        860        870
LAV BRU  RIVELLGRRG WEALKYWWNL LQYWSQELKN SAVSLLNATA IAVAEGTDRV IEVVQGACRA IRHIPRRIRQ GLERILL
ARV 2     T  I  K           S      I          W         T          A R Y    L  H          L
LAV MAL                  L        G        I    T        C       IG RFG    L          F  A
LAV ELI              DI   L            R    S  FD I               II R     VLN            S
```

FIG. 3F-1

F

```
                   10          20          30          40          50          60          70          80
LAV BRU   MGGKWSKSSV  VGWPTVRERM  R----RAEPA  ADGVGAASR-  ----DLEKUG  AITSSNTAAT  NAACAWLEAQ  EE-EEVGFPV
ARV 2            R M  G  SAI       RAEP              V  -  ----                     D           -
LAV MAL            I      KI   I   ---- TP T  ET    VQD   AVSQ  D C    AA SP   N    S --- PP     E
LAV ELI            I      AI   I   ---- TM           V  -  ----                 S    D           SD

                   90         100         110         120         130         140         150         160
LAV BRU   TPQVPLRRHT  YKAAVDLSHF  LKEKGGLEGL  IHSQRRQDIL  DLWIYUTQGY  FPDWQNYTPC  PGVRYPLTFG  WCYKLVPVEP
ARV 2     R               L  I                 W     E                                I           F
LAV MAL   R             G F              D    VW PK  E       V                        I F         F   HS
LAV ELI   R             E L                    W KK  E       V N  I                   I            E   D

                  170         180         190         200         210
LAV BRU   DKVEEANKGE  NTSLLHPVSL  HGMDDPEREV  LEWRFDSRLA  FHHVARELHP  EYFKNC
ARV 2     E      E     N     M       E A K     V     K       M          Y D
LAV MAL   EE     E     NC    I Q     E A       K K   S    LR R   Q      Y D
LAV ELI   QE   DTE    TN     ICQ     E   Q     K   N       E K   M     FY  -
```

FIG. 3F–2

FIG. 4A

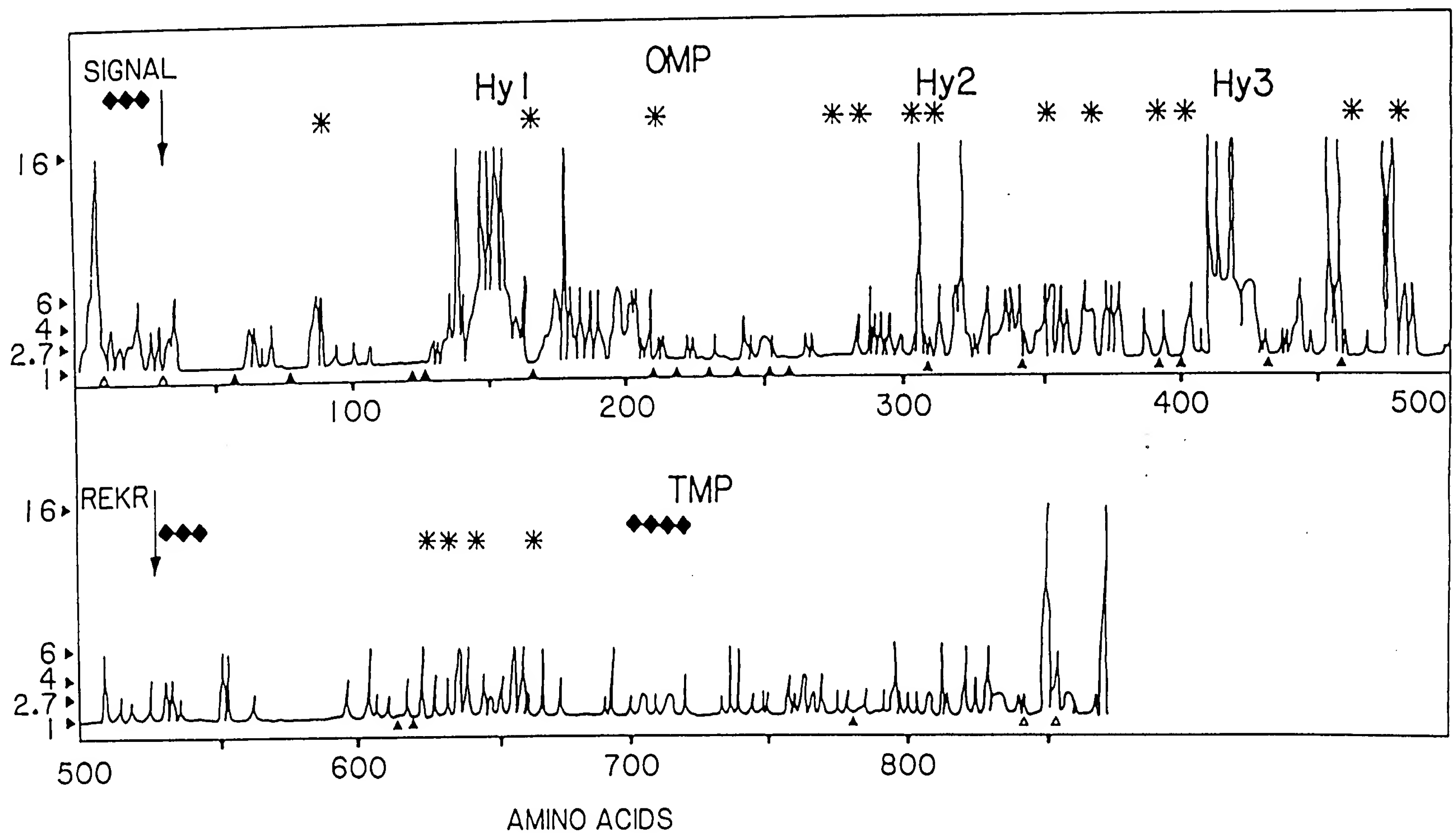
A LAVbru vs.	GAG		POL		ENV TOTAL		ENV OMP		ENV TMP	
HTLV-3 USA	512 0/0	0.8	1015 0/0	1.3	856 5/0	1.4	507 5/0	1.6	349 0/0	1.1
ARV-2 USA	502 12/2	3.4	1003 12/0	3.1	855 17/11	13.0	505 17/10	14.3	350 0/1	11.2
LAVeli ZAIRE	500 13/1	9.8	1002 13/0	5.5	853 22/14	20.7	504 22/14	25.3	349 0/0	13.8
LAVmal ZAIRE	505 14/7	12.0	1002 13/0	7.7	859 13/11	21.7	509 13/10	26.4	350 0/1	14.9

B LAVeli vs.	GAG		POL		ENV TOTAL		ENV OMP		ENV TMP	
LAVmal	505 1/6	10.8	1002 0/0	8.4	859 13/11	19.8	509 8/13	23.6	350 0/1	14.3

FIG. 4B

A LAVbru vs.	orf F		central region					
			orf Q		orf R		orf S	
HTLV-3 USA	206 0/0	1.5	192 0/0	0		nd	80 0/0	2.5
ARV-2 USA	210 0/4	12.6	192 0/0	10.0	97 0/1	9.4	81 0/1	15.0
LAVeli ZAIRE	206 1/1	19.4	192 0/0	10.4	96 0/0	11.5	80 0/0	27.5
LAVmal ZAIRE	209 2/5	27.0	192 0/0	12.6	96 0/0	10.4	80 0/0	23.8
B LAVeli vs.								
LAVmal	209 3/6	22.5	192 0/0	12.0	96 0/0	6.3	80 0/0	11.3

FIG. 5



SIGNAL
OMP
Hy1
Hy2
Hy3
16
6
4
2.7
1
100
200
300
400
500
REKR
TMP
600
700
800
AMINO ACIDS

GAG

a

```
                                  120
            K   A   Q   Q   A   A   A                        D   T
LAV.BRU    AAA GCA CAG CAA GCA GCA GCT    -   -   -   -   - GAC ACA

            K   A   Q   Q   A   A   A   A   A -   -   -   -  G   T
ARV 2      AAG GCA CAG CAA GCA GCA GCT GCA GCT              GGC ACA

            K   T   Q   Q   A   A   A   A   Q   Q   A   A   A   A   T
LAV.MAL    AAG ACA[CAG CAG GCA GCA GCT GCA][CAG CAG GCA GCA GCT GCC]ACA

            X   A   Q   Q   A   A   A                            D   T
LAV.ELI    AAG GCA CAG CAA GCA GCA GCT -   -   -   -   -   -    GAC ACA
```

FIG. 6A-1

```
.BRU
                         460                                                           470                                                    480
 N    F   L   Q   S   R   P   E   P   T   A   P   P    F   L   Q   S   R   P   E   P   T   A   P   P    E   E
AAT |TTT CTT CAG AGC AGA CCA GAG CCA ACA GCC CCA CCA| |TTT CTT CAG AGC AGA CCA GAG CCA ACA GCC CCA CCA| GAA GAG

2
 N    F   L   Q   S   R   P   E   P   T   A   P   P                                                       E   E
AAT  TTT CTT CAG AGC AGA CCA GAG CCA ACA GCC CCA CCA  -   -   -   -   -   -   -   -   -   -   -   -     GAA GAG

.MAL
 N    F   L   Q   S   R   P   E   P   T   A   P   P                                                       A   E
AAT  TTC CTT CAG AGC AGA CCA GAG CCA ACA GCC CCA CCA  -   -   -   -   -   -   -   -   -   -   -   -     GCA GAG

.ELI
 N    F   L   Q   S   R   P   E   P   T   A   P   P                                                       A   E
AAC  TTT CTC CAA AGC AGA CCA GAG CCA ACA GCC CCA CCA  -   -   -   -   -   -   -   -   -   -   -   -     GCA GAG
```

FIG. 6A-2

```
c
                  20                                          30
           R   M   R                     R   A   E   P   A
LAV.BRU   AGA ATG AGA  -   -   -   -   CGA GCT GAG CCA GCA

           R   M   R   R   A   E   P   R   A   E   P   A
ARV 2     AGA ATG AGA CGA GCT GAG CCA CGA GCT GAG CCA GCA

           R   I   R                     R   T   P   P   T
LAV.MAL   AGA ATA AGA  -   -   -   -   CGA ACT CCC CCA ACA

           R   I   R                     R   T   P   P   T
LAV.ELI   AGA ATA AGA  -   -   -   -   AGA ACT AAT CCA GCA

d
                              40
           V   G   A   A   S   R                         D
LAV.BRU   GTG GGA GCA GCA TCT CGA  -   -   -   -   -   - GAC

           V   G   A   V   S   R                         D
ARV 2     GTG GGA GCA GTA TCT CGA  -   -   -   -   -   - GAC

           V   G   A   V   S   R   D   A   V   S   Q   D
LAV.MAL   GTA GGA GCA GTA TCT CAA GAT GCA GTA TCT CAA GAT

           V   G   A   V   S   R                         D
LAV.ELI   GTA GGA GCA GTA TCT CGA  -   -   -   -   -   - GAC
```

FIG. 6A-3

ENV

e

```
                                                  20
             Q   H   L    W   R   W   G    W   K   W   G    T   M   L
LAV.BRU     CAG CAC TTG [TGG ACA TGG GGC][TGG AAA TGG GGC] ACC ATG CTC

             Q   H   L   W   R   W   G                      T   L   L
ARV 2       CAG CAC TTG TGG AGA TGG GGC   -   -   -   -    ACC TTG CTC

             Q   N   W   W   R   W   G                      M   M   L
LAV.MAL     CAA AAC TGG TGG AGA TGG GGC   -   -   -   -    ATG ATG CTC

             Q   N   W   W   K   W   G                      T   M   L
LAV.ELI     CAA AAC TGG TGG AAA TCG GGC   -   -   -   -    ATC ATG CTC
```

FIG. 6B-1

f

```
LAV.BRU                          140                                             150
 L   K   C   T   D   L       G   N   A   T    N   T   N   S   S    N   T   N   S   S    S   G   E
TTA AAG TGC ACT GAT TTG  -  GGG AAT GCT ACT [AAT ACC AAT AGT AGT][AAT ACC AAT AGT AGT] AGC GGG GAA

 M   M   M   E       K   G   E   I
ATG ATG ATG GAG  -  AAA GCA GAG ATA

ARV 2
 L   N   C   T   D   L       G   K   A   T   N   T   N   S   S                                  M
TTA AAT TGC ACT GAT TTG  -  GGG AAG GCT ACT AAT ACC AAT AGT AGT  -   -   -   -   -   -   -   AAT

 W    K   E   E   I    K   G   E   I
TGG [AAA GAA GAA ATA][AAA GGA GAA ATA]
```

```
LAV.MAL
 L   N   C   T  | N   V   N   G   T | A   V   N   G   T | N   A   G | S   N   R   T   N   A   E
TTA AAC TGC ACT |AAT GTG AAT GGG ACT|GCT GTG AAT GGG ACT|AAT GCT GGG|AGT AAT AGG ACT AAT GCA GAA

 L   K   M   E   I       G   E   V
TTG AAA ATG GAA ATT  -  GGA GAA GTG

LAV.ELI
 L   N   C   S   D   E          | L   R   N   N   G   T | M   G   N   N   V   T | T   E   E   K
TTA AAC TGT AGT GAT GAA  -   -  |TTG AGG AAC AAT GGC ACT|ATG GGG AAC AAT GTC ACT|ACA GAG GAG AAA

 G                               M
GGA  -   -   -   -   -   -   -  ATG
```

FIG. 6B–2

```
g                                  200
            D   N   D   T   T   S                      Y   T   L
LAV.BRU    GAT AAT GAT ACT ACC AGC -   -   -   -   -  TAT ACG TTG

            D   N   A   S   T   T   T   N   Y   T   N   Y   R   L
ARV 2      GAT AAT GCT AGT ACT ACT|ACC AAC TAT|ACC AAC TAT|AGG TTG

            D   D   S   D   N   S   S                  Y   R   L
LAV.MAL   |GAT GAT AGT|GAT AAT AGT|AGT -   -   -   -  TAT AGG CTA

            D   N   D   S   S   T       N   S   T   N   Y   R   L
LAV.ELI    GAC AAT GAT AGT|AGT ACC  -  AAT|AGT ACC AAT|TAT AGG TTA
```

FIG. 6B-3

```
h
LAV.BRU                    410                                     420
 C   N   S   T   Q   L   F   N   S   T   W   F   N   S   T   W   S   T   E   G   S   N   N   T   E   G
TGT AAT TCA ACA CAA CTG|TTT AAT AGT ACT TGG|TTT AAT AGT ACT TGG|AGT ACT GAA GGG TCA AAT AAC ACT GAA GGA
        430
 S   D   T   I
AGT GAC ACA ATC

ARV 2
 C   N   T   T   Q   L   F   N   N   T   W                       R   L   N   H   T   K   G   T   K   G
TGT AAT ACA ACA CAA CTG TTT AAT AAT ACA TGG -   -   -   -   -   AGG TTA AAT CAC|ACT GAA GGA|ACT AAA GGA|

 N   D   T   I
AAT GAC ACA ATC
```

```
LAV.MAL

 C   N   T   S   K   L   F   N   S   T   W   Q   N   N   G   A   R   L           S   N   S   T   E   S
TGT AAT ACA TCA AAA CTG TTT AAT AGT ACA TGG CAG AAT AAT GGT GCA AGA CTA  -   -  AGT AAT AGC ACA GAG TCA

 T   G   S   I
ACT GGT AGT ATC

LAV.ELI

 C   N   T   S   G   L   F   N   S   T   W   N   I   S   A   W   N   N   I   T   E   S   N   N   S   T
TGT AAT ACA TCA GGA CTG TTT AAT AGT ACA TGG AAT ATT AGT GCA TGG AAT AAT ATT ACA GAG TCA AAT AAT AGC ACA

 N   T   N   I
AAC ACA AAC ATC
```

FIG. 6B–4

LAV.ELI

→R
GGTCTCTCTGGTTAGACCAGATTTGAGCCTGGGAGCTCTCTGGCTAGCTAGGGAACCCAC
R ←→ U5
TGCTTAAGCCTCAATAAAGCTTGCCTTGAGTGCTTCAAGTAGTGTGTGCCCGTCTGTTGT
100
GTGACTCTGGTAACTAGAGATCCCTCAGACCCTTTTAGTCAGAGTGGAAAATCTCTAGCA
U5←
GTGGCGCCCGAACAGGGACCTGAAAGCGAAAGTAGAACCAGAGGAGCTCTCTCGACGCAG
200
GACTCGGCTTGCTGAAGCGCGCACGGCAAGAGGCGAGGGGCAGCGACTGGTGAGTACGCT
→GAG. 300
MetGlyAlaArgAlaSerValLeuSer
AAAATTTTTGACTAGCGGAGGCTAGAAGGAGAGAGATGGGTGCGAGAGCGTCAGTATTAA

GlyGlyLysLeuAspLysTrpGluLysIleArgLeuArgProGlyGlyLysLysLysTyr
GCGGGGGAAAATTAGATAAATGGGAAAAAATTCGGTTACGGCCAGGAGGAAAGAAAAAAT
400
ArgLeuLysHisIleValTrpAlaSerArgGluLeuGluArgTyrAlaLeuAsnProGly
ATAGACTAAAACATATAGTATGGGCAAGCAGGGAGCTAGAACGATATGCACTTAATCCTG

LeuLeuGluThrSerGluGlyCysLysGlnIleIleGlyGlnLeuGlnProAlaIleGln
GCCTTTTAGAAACATCAGAAGGCTGTAAACAAATAATAGGGCAGCTACAACCAGCTATTC
500
ThrGlyThrGluGluLeuArgSerLeuTyrAsnThrValAlaThrLeuTyrCysValHis
AGACAGGAACAGAAGAACTTAGATCATTATATAATACAGTAGCAACCCTCTATTGTGTAC
600
LysGlyIleAspValLysAspThrLysGluAlaLeuGluLysMetGluGluGluGlnAsn
ATAAAGGAATAGATGTAAAAGACACCAAGGAAGCTTTAGAAAAGATGGAGGAAGAGCAAA

LysSerLysLysLysAlaGlnGlnAlaAlaAlaAspThrGlyAsnAsnSerGlnValSer
ACAAAAGTAAGAAAAAAGGCACAGCAAGCAGCAGCTGACACAGGAAACAACAGCCAGGTCA
700
GlnAsnTyrProIleValGlnAsnLeuGlnGlyGlnMetValHisGlnAlaIleSerPro
GCCAAAATTATCCTATAGTGCAGAACCTACAGGGGCAAATGGTACATCAGGCCATATCAC

ArgThrLeuAsnAlaTrpValLysValIleGluGluLysAlaPheSerProGluValIle
CTAGAACTTTGAACGCATGGGTAAAAGTAATAGAAGAAAAGGCTTTCAGCCCAGAAGTAA
800
ProMetPheSerAlaLeuSerGluGlyAlaThrProGlnAspLeuAsnThrMetLeuAsn
TACCCATGTTTTCAGCATTATCAGAAGGAGCCACCCCACAAGATTTAAACACCATGCTAA
900
ThrValGlyGlyHisGlnAlaAlaMetGlnMetLeuLysGluThrIleAsnGluGluAla
ACACAGTGGGGGGACATCAAGCAGCCATGCAAATGCTAAAAGAGACCATCAATGAAGAAG

AlaGluTrpAspArgLeuHisProValHisAlaGlyProIleAlaProGlyGlnMetArg
CTGCAGAATGGGATAGGTTACATCCAGTGCATGCAGGGCCTATTGCACCAGGCCAGATGA
1000
GluProArgGlySerAspIleAlaGlyThrThrSerThrLeuGlnGluGlnIleAlaTrp
GAGAACCAAGGGGAAGTGATATAGCAGGAACTACTAGTACCCTTCAGGAACAAATAGCAT

MetThrSerAsnProProIleProValGlyGluIleTyrLysArgTrpIleIleValGly
GGATGACAAGTAACCCACCTATCCCAGTAGGAGAAATCTATAAAAGATGGATAATTGTGG
1100
LeuAsnLysIleValArgMetTyrSerProValSerIleLeuAspIleArgGlnGlyPro
GATTAAATAAAATAGTAAGAATGTATAGCCCTGTCAGCATTTTGGACATAAGACAGGGAC
1200

FIG. 7A

LysGluProPheArgAspTyrValAspArgPheTyrLysThrLeuArgAlaGluGlnAla
CAAAGGAACCTTTTAGAGACTATGTAGACCGGTTCTATAAAACTCTAAGAGCCGAGCAAG

SerGlnAspValLysAsnTrpMetThrGluThrLeuLeuValGlnAsnAlaAsnProAsp
CTTCACAGGATGTAAAAAATTGGATGACAGAAACCTTGTTGGTCCAAAATGCAAACCCAG
1300
CysLysThrIleLeuLysAlaLeuGlyProGlnAlaThrLeuGluGluMetMetThrAla
ATTGCAAGACTATCTTAAAAGCATTGGGACCACAGGCTACACTAGAAGAAATGATGACAG

CysGlnGlyValGlyGlyProSerHisLysAlaArgValLeuAlaGluAlaMetSerGln
CATGTCAGGGAGTGGGGGGCCCAGCCATAAAGCAAGAGTTCTGGCTGAGGCAATGAGCC
1400
AlaThrAsnSerValThrThrAlaMetMetGlnArgGlyAsnPheLysGlyProArgLys
AAGCAACAAATTCAGTTACTACAGCAATGATGCAGAGAGGCAATTTTAAGGGCCCAAGAA
1500
IleIleLysCysPheAsnCysGlyLysGluGlyHisIleAlaLysAsnCysArgAlaPro
AAATTATTAAGTGTTTCAATTGTGGCAAAGAAGGGCACATAGCAAAAAATTGCAGGGCCC

ArgLysLysGlyCysTrpArgCysGlyLysGluGlyHisGlnLeuLysAspCysThrGlu
CTAGGAAAAAGGGCTGTTGGAGATGTGGAAAGGAAGGACACCAACTAAAAGATTGCACTG
→POL 1600
PhePheArgGluAsnLeuAlaPheProGlnGlyLysAlaGlyGluLeu
ArgGlnAlaAsnPheLeuGlyArgIleTrpProSerHisLysGlyArgProGlyAsnPhe
AGAGACAGGCTAATTTTTTAGGGAGAATTTGGCCTTCCCACAAGGGAAGGCCGGGGAACT

SerProLysGlnThrArgAlaAsnSerProThrSerArgGluLeuArgValTrpGlyArg
LeuGlnSerArgProGluProThrAlaProProAlaGluSerPheGlyPheGlyGluGlu
TTCTCCAAAGCAGACCAGAGCCAACAGCCCCACCAGCAGAGAGCTTCGGGTTTGGGGAAG
1700
AspAsnProLeuSerLysThrGlyAlaGluArgGlnGlyThrValSerPheAsnPhePro
IleThrProSerGlnLysGlnGluGlnLysAspLysGluLeuTyrProLeuThrSerLeu
AGATAACCCCCTCTCAAAAACAGGAGCAGAAAGACAAGGAACTGTATCCTTTAACTTCCC
.GAG← 1800
GlnIleThrLeuTrpGlnArgProLeuValAlaIleLysIleGlyGlyGlnLeuLysGlu
LysSerLeuPheGlyAsnAspProLeuSerGln
TCAAATCACTCTTTGGCAACGACCCCTTGTCGCAATAAAAATAGGGGGACAGCTAAAGGA

AlaLeuLeuAspThrGlyAlaAspAspThrValLeuGluGluMetAsnLeuProGlyLys
AGCTCTATTAGATACAGGAGCAGATGATACAGTATTAGAAGAAATGAATTTGCCAGGAAA
1900
TrpLysProLysMetIleGlyGlyIleGlyGlyPheIleLysValArgGlnTyrAspGln
ATGGAAACCAAAAATGATAGGGGGAATTGGAGGTTTTATCAAAGTAAGACAGTATGATCA

IleProIleGluIleCysGlyGlnLysAlaIleGlyThrValLeuValGlyProThrPro
AATACCCATAGAAATCTGTGGACAGAAAGCTATAGGTACAGTATTAGTAGGACCTACGCC
2000
ValAsnIleIleGlyArgAsnLeuLeuThrGlnIleGlyCysThrLeuAsnPheProIle
TGTCAACATAATCGGAAGAAATTTGTTGACCCAGATTGGCTGCACTTTAAATTTTCCAAT
2100
SerProIleGluThrValProValLysLeuLysProGlyMetAspGlyProLysValLys
TAGTCCTATTGAAACTGTACCAGTAAAATTAAAGCCAGGAATGGATGGCCCAAAAGTTAA

GlnTrpProLeuThrGluGluLysIleLysAlaLeuThrGluIleCysThrAspMetGlu
ACAATGGCCATTGACAGAAGAAAAAATAAAAGCATTAACAGAAATTTGTACAGATATGGA
2200

FIG. 7B

LysGluGlyLysIleSerArgIleGlyProGluAsnProTyrAsnThrProIlePheAla
AAAGGAAGGAAAAATTTCAAGAATTGGGCCTGAAAATCCATACAATACTCCAATATTTGC

IleLysLysLysAspSerThrLysTrpArgLysLeuValAspPheArgGluLeuAsnLys
CATAAAGAAAAAAGACAGTACCAAGTGGAGAAAATTAGTAGATTTCAGAGAACTTAATAA
2300

ArgThrGlnAspPheTrpGluValGlnLeuGlyIleProHisProAlaGlyLeuLysLys
GAGAACTCAAGATTTCTGGGAAGTTCAATTAGGAATACCGCATCCTGCAGGGCTGAAAAA
2400

LysLysSerValThrValLeuAspValGlyAspAlaTyrPheSerValProLeuAspGlu
GAAAAAATCAGTAACAGTACTGGATGTGGGTGATGCATATTTTTCAGTTCCCTTAGATGA

AspPheArgLysTyrThrAlaPheThrIleSerSerIleAsnAsnGluThrProGlyIle
AGATTTTAGGAAATATACCGCCTTTACCATATCTAGTATAAACAATGAGACACCAGGGAT
2500

ArgTyrGlnTyrAsnValLeuProGlnGlyTrpLysGlySerProAlaIlePheGlnSer
TAGATATCAGTACAATGTGCTTCCACAGGGATGGAAAGGATCACCGGCAATATTCCAAAG

SerMetThrLysIleLeuGluProPheArgLysGlnAsnProGluMetValIleTyrGln
TAGCATGACAAAAATCTTAGAGCCCTTTAGAAAACAAAATCCAGAAATGGTTATCTATCA
2600

TyrMetAspAspLeuTyrValGlySerAspLeuGluIleGlyGlnHisArgThrLysIle
ATACATGGATGATTTGTATGTAGGATCTGACTTAGAAATAGGGCAGCATAGGACAAAAAT
2700

GluLysLeuArgGluHisLeuLeuArgTrpGlyPheThrArgProAspLysLysHisGln
AGAGAAATTAAGAGAACATCTATTGAGGTGGGGATTTACCAGACCAGATAAAAAACATCA

LysGluProProPheLeuTrpMetGlyTyrGluLeuHisProAspLysTrpThrValGln
GAAAGAACCCCCATTTCTTTGGATGGGTTATGAACTCCATCCTGATAAATGGACAGTACA
2800

SerIleLysLeuProGluLysGluSerTrpThrValAsnAspIleGlnAsnLeuValGlu
GTCTATAAAACTGCCAGAAAAGGAGAGCTGGACTGTCAATGATATACAGAACTTAGTGGA

ArgLeuAsnTrpAlaSerGlnIleTyrProGlyIleLysValArgGlnLeuCysLysLeu
GAGATTAAACTGGGCAAGCCAGATTTATCCAGGAATTAAAGTAAGACAATTATGTAAACT
2900

LeuArgGlyThrLysAlaLeuThrGluValIleProLeuThrGluGluAlaGluLeuGlu
CCTTAGGGGAACCAAAGCACTAACAGAAGTAATACCACTAACAGAAGAAGCAGAATTAGA
3000

LeuAlaGluAsnArgGluIleLeuLysGluProValHisGlyValTyrTyrAspProSer
ACTGGCAGAAAACAGGGAAATTTTAAAAGAACCAGTACATGGAGTGTATTATGACCCATC

LysAspLeuIleAlaGluIleGlnLysGlnGlyHisGlyGlnTrpThrTyrGlnIleTyr
AAAAGACTTAATAGCAGAAATACAGAAACAAGGGCACGGCCAATGGACATACCAAATTTA
3100

GlnGluProPheLysAsnLeuLysThrGlyLysTyrAlaArgMetArgGlyAlaHisThr
TCAAGAACCATTTAAAAATCTGAAAACAGGAAAGTATGCAAGAATGAGGGGTGCCCACAC

AsnAspValLysGlnLeuAlaGluAlaValGlnArgIleSerThrGluSerIleValIle
TAATGATGTAAAGCAATTAGCAGAGGCAGTGCAAAGAATATCCACAGAAAGCATAGTGAT
3200

TrpGlyArgThrProLysPheArgLeuProIleGlnLysGluThrTrpGluThrTrpTrp
ATGGGGAAGGACTCCTAAATTTAGACTACCCATACAAAAGGAAACATGGGAAACATGGTG
3300

FIG. 7C

AlaGluTyrTrpGlnAlaThrTrpIleProGluTrpGluPheValAsnThrProProLeu
GGCAGAGTATTGGCAAGCCACTTGGATTCCTGAGTGGGAATTTGTCAATACCCCTCCTTT

ValLysLeuTrpTyrGlnLeuGluLysGluProIleIleGlyAlaGluThrPheTyrVal
AGTAAAATTATGGTACCAGTTAGAGAAGGAACCCATAATAGGAGCAGAAACTTTCTATGT
3400

AspGlyAlaAlaAsnArgGluThrLysLeuGlyLysAlaGlyTyrValThrAspArgGly
AGATGGGGCAGCTAATAGAGAGACTAAATTAGGAAAAGCAGGATATGTTACTGACAGAGG

ArgGlnLysValValProLeuThrAspThrThrAsnGlnLysThrGluLeuGlnAlaIle
AAGACAGAAAGTTGTCCCTTTGACTGACACGACAAATCAGAAGACTGAGTTACAAGCAAT
3500

AsnLeuAlaLeuGlnAspSerGlyLeuGluValAsnIleValThrAspSerGlnTyrAla
TAATCTAGCCTTGCAGGATTCGGGATTAGAAGTAAACATAGTAACAGATTCACAATATGC
3600

LeuGlyIleIleGlnAlaGlnProAspLysSerGluSerGluLeuValAsnGlnIleIle
ATTAGGAATCATTCAAGCACAACCAGATAAGAGTGAATCAGAGTTAGTCAATCAAATAAT

GluGlnLeuIleLysLysGluLysValTyrLeuAlaTrpValProAlaHisLysGlyIle
AGAGCAGTTAATAAAAAAGGAAAAGGTTTACCTGGCATGGGTACCAGCACACAAAGGAAT
3700

GlyGlyAsnGluGlnValAspLysLeuValSerGlnGlyIleArgLysValLeuPheLeu
TGGAGGAAATGAACAAGTAGATAAATTAGTCAGTCAAGGAATCAGGAAAGTACTATTTTT

AspGlyIleAspLysAlaGlnGluGluHisGluLysTyrHisAsnAsnTrpArgAlaMet
GGATGGAATAGATAAGGCTCAAGAAGAACATGAGAAATATCACAACAATTGGAGAGCAAT
3800

AlaSerAspPheAsnLeuProProValValAlaLysGluIleValAlaSerCysAspLys
GGCTAGTGATTTTAACCTACCACCCGTGGTAGCAAAAGAAATAGTAGCTAGCTGTGATAA
3900

CysGlnLeuLysGlyGluAlaMetHisGlyGlnValAspCysSerProGlyIleTrpGln
ATGTCAGCTAAAAGGAGAAGCCATGCATGGACAAGTAGACTGTAGTCCAGGAATATGGCA

LeuAspCysThrHisLeuGluGlyLysValIleLeuValAlaValHisValAlaSerGly
ATTAGATTGTACACACTTAGAAGGAAAAGTTATCCTGGTAGCAGTTCATGTAGCCAGTGG
4000

TyrIleGluAlaGluValIleProAlaGluThrGlyGlnGluThrAlaTyrPheLeuLeu
CTATATAGAAGCAGAAGTTATTCCAGCAGAAACAGGGCAGGAAACAGCATATTTTCTTTT

LysLeuAlaGlyArgTrpProValLysValValHisThrAspAsnGlySerAsnPheThr
AAAATTAGCAGGAAGATGGCCAGTAAAAGTAGTACATACAGACAATGGCAGCAATTTCAC
4100

SerAlaAlaValLysAlaAlaCysTrpTrpAlaGlyIleLysGlnGluPheGlyIlePro
CAGTGCTGCAGTTAAGGCCGCCTGTTGGTGGGCAGGTATCAAACAGGAATTTGGAATTCC
4200

TyrAsnProGlnSerGlnGlyValValGluSerMetAsnLysGluLeuLysLysIleIle
CTACAATCCCCAAAGTCAAGGAGTAGTAGAATCTATGAATAAAGAATTAAAGAAAATTAT

GlyGlnValArgAspGlnAlaGluHisLeuLysThrAlaValGlnMetAlaValPheIle
AGGACAGGTAAGAGATCAAGCTGAACATCTTAAGACAGCAGTACAAATGGCAGTATTCAT
4300

HisAsnPheLysArgArgArgGlyIleGlyGlyTyrSerAlaGlyGluArgIleIleAsp
CCACAATTTTAAAAGAAGAAGGGGGATTGGGGGATACAGTGCAGGGGAAAGAATAATAGA

FIG. 7D

IleIleAlaThrAspIleGlnThrLysGluLeuGlnLysGlnIleIleLysIleGlnAsn
CATAATAGCAACAGACATACAAACTAAAGAATTACAAAAACAAATTATAAAAATTCAAAA
4400

PheArgValTyrTyrArgAspSerArgAspProIleTrpLysGlyProAlaLysLeuLeu
TTTTCGGGTTTATTACAGAGACAGCAGAGATCCAATTTGGAAAGGACCAGCAAAGCTCCT
4500

TrpLysGlyGluGlyAlaValValIleGlnAspLysSerAspIleLysValValProArg
CTGGAAAGGTGAAGGGGCAGTAGTAATACAAGACAAGAGTGACATAAAGGTAGTACCAAG

→Q
ArgLysValLysIleIleArgAspTyrGlyLysGlnMetAlaGlyAspAspCysValAla
MetGluAsnArgTrpGlnValMetIleValTrpGln
AAGAAAAGTAAAGATTATTAGGGATTATGGAAAACAGATGGCAGGTGATGATTGTGTGGC
4600

POL←
SerArgGlnAspGluAsp
ValAspArgMetArgIleLysThrTrpLysSerLeuValLysHisHisMetTyrValSer
AAGTAGACAGGATGAGGATTAAAACATGGAAAAGTTTAGTAAAACACCATATGTATGTTT

LysLysAlaAsnArgTrpPheTyrArgHisHisTyrGluSerProHisProLysIleSer
CAAAGAAAGCTAACAGATGGTTTTATAGACATCACTATGAAAGCCCCCACCCAAAAATAA
4700

SerGluValHisIleProLeuGlyGluAlaArgLeuValIleLysThrTyrTrpGlyLeu
GTTCAGAAGTACACATCCCACTAGGAGAAGCTAGACTGGTAATAAAAACATATTGGGGTC
4800

HisThrGlyGluArgGluTrpHisLeuGlyGlnGlyValSerIleGluTrpArgLysArg
TGCATACAGGAGAAAGAGAATGGCATCTGGGTCAGGGAGTCTCCATAGAATGGAGGAAAA

ArgTyrSerThrGlnValAspProGlyLeuAlaAspGlnLeuIleHisMetTyrTyrPhe
GGAGATATAGCACACAAGTAGACCCTGGCCTGGCAGACCAACTAATTCATATGTATTATT
4900

AspCysPheSerGluSerAlaIleArgLysAlaIleLeuGlyAspIleValSerProArg
TTGATTGTTTTTCAGAATCTGCTATAAGAAAAGCCATATTAGGAGATATAGTTAGTCCTA

CysGluTyrGlnAlaGlyHisAsnLysValGlySerLeuGlnTyrLeuAlaLeuThrAla
GGTGTGAGTATCAAGCAGGACATAACAAGGTAGGATCCCTACAGTATTTGGCACTAACAG
5000

LeuIleAlaProLysGlnIleLysProProLeuProSerValArgLysLeuThrGluAsp
CATTAATAGCACCAAAACAGATAAAGCCACCTTTGCCTAGTGTTAGGAAGCTAACAGAAG
5100

→R
MetGluGlnAlaProAlaAspGlnGlyProGlnArgGluProTyrAsnGluTrpAla
ArgTrpAsnLysProGlnGlnThrArgGlyHisArgGlySerHisThrMetAsnGlyHis
ATAGATGGAACAAGCCCCAGCAGACCAGGGGCCACAGAGGGAGCCATACAATGAATGGGC

Q←
LeuGluLeuLeuGluGluLeuLysSerGluAlaValArgHisPheProArgIleTrpLeu
ATTAGAGCTTTTAGAGGAGCTTAAGAGTGAAGCTGTTAGACATTTTCCTAGGATATGGCT
5200

HisSerLeuGlyGlnHisIleTyrGluThrTyrGlyAspThrTrpValGlyValGluAla
CCATAGCTTAGGACAACATATTTATGAAACTTATGGGGATACCTGGGTAGGAGTTGAAGC

IleIleArgIleLeuGlnGlnLeuLeuPheIleHisPheArgIleGlyCysGlnHisSer
TATAATAAGAATACTGCAACAATTACTGTTTATTCATTTCAGAATTGGGTGTCAACATAG
5300

→S R←
ArgIleGlyIleIleArgGlnArgArgAlaArgAsnGlySerSerArgSer
MetAspProValAspProAsnLeuGlu
CAGAATAGGCATTATTCGACAGAGAAGAGCAAGAAATGGATCCAGTAGATCCTAACCTAG
5400

FIG. 7E

ProTrpAsnHisProGlySerGlnProArgThrProCysAsnLysCysHisCysLysLys
AGCCCTGGAACCATCCAGGAAGTCAGCCTAGGACTCCTTGTAACAAGTGTCATTGTAAAA

CysCysTyrHisCysProValCysPheLeuAsnLysGlyLeuGlyIleSerTyrGlyArg
AGTGTTGCTATCATTGCCCAGTTTGCTTCTTAAACAAAGGCTTAGGCATCTCCTATGGCA
5500

LysLysArgArgGlnArgArgGlyProProGlnGlyGlyGlnAlaHisGlnValProIle
GGAAGAAGCGGAGACAGCGACGAGGACCTCCTCAAGGCGGTCAGGCTCATCAAGTTCCTA

S ←
ProLysGln
TACCAAAGCAGTAAGTAGTACATGTAATGCAACCTTTAGGGATAATAGCAATAGCAGCAT
5600

TAGTAGTAGCAATAATACTAGCAATAGTTGTGTGGACCATAGTATTCATAGAATATAGAA
5700

GGATAAAAAAGCAAAGGAGAATAGACTGTTTACTTGATAGAATAACAGAAAGAGCAGAAG

→ ENV
MetArgAlaArgGlyIleGluArgAsnCysGlnAsnTrpTrpLysTrpGly
ACAGTGGCAATGAGAGCGAGGGGGATAGAGAGAAATTGTCAAAACTGGTGGAAATGGGGC
5800

IleMetLeuLeuGlyIleLeuMetThrCysSerAlaAlaAspAsnLeuTrpValThrVal
ATCATGCTCCTTGGGATATTGATGACCTGTAGTGCTGCAGACAATCTGTGGGTCACAGTT

TyrTyrGlyValProValTrpLysGluAlaThrThrThrLeuPheCysAlaSerAspAla
TATTATGGGGTGCCTGTATGGAAGGAAGCAACCACCACTCTATTTTGTGCATCAGATGCT
5900

LysSerTyrGluThrGluAlaHisAsnIleTrpAlaThrHisAlaCysValProThrAsp
AAATCATATGAAACAGAGGCACATAATATCTGGGCCACACATGCCTGTGTACCCACGGAC
6000

ProAsnProGlnGluIleAlaLeuGluAsnValThrGluAsnPheAsnMetTrpLysAsn
CCCAACCCACAAGAAATAGCACTGGAAAATGTGACAGAAAACTTTAACATGTGGAAAAAT

AsnMetValGluGlnMetHisGluAspIleIleSerLeuTrpAspGlnSerLeuLysPro
AACATGGTGGAACAGATGCATGAGGATATAATCAGTTTATGGGATCAAAGCCTAAAACCA
6100

CysValLysLeuThrProLeuCysValThrLeuAsnCysSerAspGluLeuArgAsnAsn
TGTGTAAAATTAACCCCACTCTGTGTCACTTTAAACTGTAGTGATGAATTGAGGAACAAT

GlyThrMetGlyAsnAsnValThrThrGluGluLysGlyMetLysAsnCysSerPheAsn
GGCACTATGGGGAACAATGTCACTACAGAGGAGAAAGGAATGAAAAACTGCTCTTTCAAT
6200

ValThrThrValLeuLysAspLysLysGlnGlnValTyrAlaLeuPheTyrArgLeuAsp
GTAACCACAGTACTAAAAGATAAGAAGCAGCAAGTATATGCACTTTTTTATAGACTTGAT
6300

IleValProIleAspAsnAspSerSerThrAsnSerThrAsnTyrArgLeuIleAsnCys
ATAGTACCAATAGACAATGATAGTAGTACCAATAGTACCAATTATAGGTTAATAAATTGT

AsnThrSerAlaIleThrGlnAlaCysProLysValSerPheGluProIleProIleHis
AATACCTCAGCCATTACACAGGCTTGTCCAAAGGTATCCTTTGAGCCAATTCCCATACAT
6400

TyrCysAlaProAlaGlyPheAlaIleLeuLysCysArgAspLysLysPheAsnGlyThr
TATTGTGCCCCAGCTGGTTTTGCGATTCTAAAGTGTAGAGATAAGAAGTTCAATGGAACA

GlyProCysThrAsnValSerThrValGlnCysThrHisGlyIleArgProValValSer
GGCCCATGCACAAATGTCAGCACAGTACAATGTACACATGGAATTAGGCCAGTGGTGTCA
6500

FIG. 7F

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ThrGlnLeuLeuLeuAsnGlySerLeuAlaGluGluGluValIleIleArgSerGluAsn
ACTCAACTGCTGTTGAATGGCAGTCTAGCAGAAGAAGAGGTCATAATTAGATCCGAAAAT
                                                        6600
LeuThrAsnAsnAlaLysAsnIleIleAlaHisLeuAsnGluSerValLysIleThrCys
CTCACAAACAATGCTAAAAACATAATAGCACATCTTAATGAATCTGTAAAAATTACCTGT

AlaArgProTyrGlnAsnThrArgGlnArgThrProIleGlyLeuGlyGlnSerLeuTyr
GCAAGGCCCTATCAAAATACAAGACAAAGAACACCTATAGGACTAGGGCAATCACTCTAT
                                        6700
ThrThrArgSerArgSerIleIleGlyGlnAlaHisCysAsnIleSerArgAlaGlnTrp
ACTACAAGATCAAGATCAATAATAGGACAAGCACATTGTAATATTAGTAGAGCACAATGG

SerLysThrLeuGlnGlnValAlaArgLysLeuGlyThrLeuLeuAsnLysThrIleIle
AGTAAAACTTTACAACAAGTAGCTAGAAAATTAGGAACCCTTCTTAACAAAACAATAATA
                    6800
LysPheLysProSerSerGlyGlyAspProGluIleThrThrHisSerPheAsnCysGly
AAGTTTAAACCATCCTCAGGAGGGGACCCAGAAATTACAACACACAGTTTTAATTGTGGA
                                                        6900
GlyGluPhePheTyrCysAsnThrSerGlyLeuPheAsnSerThrTrpAsnIleSerAla
GGGGAATTCTTCTACTGTAATACATCAGGACTGTTTAATAGTACATGGAATATTAGTGCA

TrpAsnAsnIleThrGluSerAsnAsnSerThrAsnThrAsnIleThrLeuGlnCysArg
TGGAATAATATTACAGAGTCAAATAATAGCACAAACACAAACATCACACTCCAATGCAGA
                                        7000
IleLysGlnIleIleLysMetValAlaGlyArgLysAlaIleTyrAlaProProIleGlu
ATAAAACAAATTATAAAGATGGTGGCAGGCAGGAAAGCAATATATGCCCCTCCTATCGAA

ArgAsnIleLeuCysSerSerAsnIleThrGlyLeuLeuLeuThrArgAspGlyGlyIle
AGAAACATTCTATGTTCATCAAATATTACAGGGCTACTATTGACAAGAGATGGTGGTATA
                    7100
AsnAsnSerThrAsnGluThrPheArgProGlyGlyGlyAspMetArgAspAsnTrpArg
AATAATAGTACTAACGAGACCTTTAGACCTGGAGGAGGAGATATGAGGGACAATTGGAGA
                                                        7200
SerGluLeuTyrLysTyrLysValValGlnIleGluProLeuGlyValAlaProThrArg
AGTGAATTATATAAATATAAGGTAGTACAAATTGAACCACTAGGAGTAGCACCCACCAGG

AlaLysArgArgValValGluArgGluLysArgAlaIleGlyLeuGlyAlaMetPheLeu
GCAAAGAGAAGAGTGGTGGAAAGAGAAAAAAGAGCAATAGGATTAGGAGCTATGTTCCTT
                                        7300
GlyPheLeuGlyAlaAlaGlySerThrMetGlyAlaArgSerValThrLeuThrValGln
GGGTTCTTGGGAGCAGCAGGAAGCACGATGGGCGCACGGTCAGTGACGCTGACGGTACAG

AlaArgGlnLeuMetSerGlyIleValGlnGlnGlnAsnAsnLeuLeuArgAlaIleGlu
GCCAGACAATTAATGTCTGGTATAGTGCAACAGCAAAACAATTTGCTGAGGGCTATAGAG
                    7400
AlaGlnGlnHisLeuLeuGlnLeuThrValTrpGlyIleLysGlnLeuGlnAlaArgIle
GCGCAACAGCATCTGTTGCAACTCACGGTCTGGGGCATTAAACAGCTCCAGGCAAGAATC
                                                        7500
LeuAlaValGluArgTyrLeuLysAspGlnGlnLeuLeuGlyIleTrpGlyCysSerGly
CTGGCTGTGGAAAGATACCTAAAGGATCAACAGCTCCTAGGAATTTGGGGTTGCTCTGGA
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FIG. 7G

LysHisIleCysThrThrAsnValProTrpAsnSerSerTrpSerAsnArgSerLeuAsn
AAACACATTTGCACCACTAATGTGCCCTGGAACTCTAGTTGGAGTAATAGATCTCTAAAT
7600

GluIleTrpGlnAsnMetThrTrpMetGluTrpGluArgGluIleAspAsnTyrThrGly
GAGATTTGGCAGAACATGACCTGGATGGAGTGGGAAAGAGAAATTGACAATTACACAGGC

LeuIleTyrSerLeuIleGluGluSerGlnThrGlnGlnGluLysAsnGluLysGluLeu
TTAATATATAGCTTAATTGAGGAATCGCAGACCCAGCAAGAAAAGAATGAAAAAGAATTG
7700

LeuGluLeuAspLysTrpAlaSerLeuTrpAsnTrpPheSerIleThrGlnTrpLeuTrp
TTGGAATTGGACAAGTGGGCAAGTTTGTGGAATTGGTTTAGCATAACACAATGGCTGTGG
7800

TyrIleLysIlePheIleMetIleIleGlyGlyLeuIleGlyLeuArgIleValPheAla
TATATAAAAATATTCATAATGATAATAGGAGGCTTGATAGGTTTAAGAATAGTTTTTGCT

ValLeuSerLeuValAsnArgValArgGlnGlyTyrSerProLeuSerPheGlnThrLeu
GTGCTTTCTTTAGTAAATAGAGTTAGGCAGGGATACTCACCTCTGTCGTTTCAGACCCTC
7900

LeuProAlaProArgGlyProAspArgProGluGlyThrGluGluGluGlyGlyGluArg
CTCCCAGCCCCGAGGGGACCCGACAGGCCCGAAGGAACAGAAGAAGAAGGTGGAGAGCGA

GlyArgAspArgSerValArgLeuLeuAsnGlyPheSerAlaLeuIleTrpAspAspLeu
GGCAGAGACAGATCCGTGAGATTGCTGAACGGATTCTCGGCACTTATCTGGGACGACCTG
8000

ArgSerLeuCysLeuPheSerTyrHisArgLeuArgAspLeuIleLeuIleAlaValArg
CGGAGCCTGTGCCTCTTCAGCTACCACCGCTTGAGAGACTTAATCTTAATTGCAGTGAGG
8100

IleValGluLeuLeuGlyArgArgGlyTrpAspIleLeuLysTyrLeuTrpAsnLeuLeu
ATTGTAGAACTTCTGGGACGCAGGGGGTGGGACATCCTCAAATATCTGTGGAATCTCCTA

GlnTyrTrpSerGlnGluLeuArgAsnSerAlaSerSerLeuPheAspAlaIleAlaIle
CAGTATTGGAGTCAGGAACTGAGGAACAGTGCTAGTAGCTTGTTTGATGCCATAGCAATA
8200

AlaValAlaGluGlyThrAspArgValIleGluIleIleGlnArgAlaCysArgAlaVal
GCAGTAGCTGAGGGGACAGATAGAGTTATAGAAATAATACAAGAGCTTGCAGAGCTGTT

W←

LeuAsnIleProArgArgIleArgGlnGlyLeuGluArgSerLeuLeu

→F

MetGlyGly

CTTAACATACCCAGAAGAATAAGACAGGGCTTAGAAAGGTCTTTACTTTAAAATGGGTGG
8300

LysTrpSerLysSerSerIleValGlyTrpProAlaIleArgGluArgIleArgArgThr
CAAATGGTCAAAAAGTAGTATAGTGGGATGGCCTGCTATAAGGGAAAGAATAAGAAGAAC
8400

AsnProAlaAlaAspGlyValGlyAlaValSerArgAspLeuGluLysHisGlyAlaIle
TAATCCAGCAGCAGATGGGGTAGGAGCAGTATCTCGAGACCTGGAAAAACATGGGGCAAT

ThrSerSerAsnThrAlaSerThrAsnAlaAspCysAlaTrpLeuGluAlaGlnGluGlu
CACAAGTAGCAATACAGCAAGTACTAATGCTGACTGTGCCTGGCTAGAAGCACAAGAAGA
8500

SerAspGluValGlyPheProValArgProGlnValProLeuArgProMetThrTyrLys
GAGCGACGAGGTGGGCTTTCCAGTCAGACCCCAGGTACCTTTAAGACCAATGACTTACAA

→U3

GluAlaLeuAspLeuSerHisPheLeuLysGluLysGlyGlyLeuGluGlyLeuIleTrp
AGAAGCTCTAGATCTCAGCCACTTTTTAAAAGAAAAGGGGGGACTGGAAGGGCTAATTTG
8600

FIG. 7H

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SerLysLysArgGlnGluIleLeuAspLeuTrpValTyrAsnThrGlnGlyIlePhePro
GTCCAAAAAGAGACAAGAGATCCTTGATCTTTGGGTCTACAACACACAAGGCATCTTCCC
                                                        8700
AspTrpGlnAsnTyrThrProGlyProGlyIleArgTyrProLeuThrPheGlyTrpCys
TGATTGGCAAAACTACACACCAGGGCCAGGGATCAGATATCCACTAACCTTTGGATGGTG

TyrGluLeuValProValAspProGlnGluValGluGluAspThrGluGlyGluThrAsn
CTACGAGCTAGTACCAGTTGATCCACAGGAGGTAGAAGAAGACACTGAAGGAGAGACCAA
                                        8800
SerLeuLeuHisProIleCysGlnHisGlyMetGluAspProGluArgGlnValLeuLys
CAGCTTGTTACACCCTATATGCCAGCATGGAATGGAGGACCCGGAGAGACAAGTGTTAAA

TrpArgPheAsnSerArgLeuAlaPheGluHisLysAlaArgGluMetHisProGluPhe
ATGGAGATTTAACAGCAGACTAGCATTTGAGCACAAGGCCCGAGAGATGCATCCGGAGTT
                  8900
TyrLysAsn
CTACAAAAACTGATGACACCGAGCTTTCTACAAGGGACTTTCCGCTGGGGACTTTCCAGG
                                                        9000
GAGGCGTGGACTGGGCGGGACTGGGGAGTGGCTAACCCTCAGATGCTGCATATAAGCAGC
                  U3←→R
TGCTTTTTGCCTGTACTGGGTCTCTCTGGTTAGACCAGATTTGAGCCTGGGAGCTCTCTG
                                        9100            B←
GCTAGCTAGGGAACCCACTGCTTAAGCCTCAATAAAGCTTGCCTTGAGTGCTTCAA
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FIG. 7I